

NOTICE OF DRAFTSPERSON'S PATENT DRAWING REVIEW

The drawing(s) filed (insert date) 01/10/06 arc:

- A. ☒ approved by the Draftsperson under 37 CFR 1.84 or 1.152.
B. ☐ objected to by the Draftsperson under 37 CFR 1.84 or 1.152 for the reasons indicated below. Corrected drawings are required.

1. DRAWINGS. 37 CFR 1.84(a): Acceptable categories of drawings: Black ink or Color (3 sets required).
Color drawings are not acceptable until petition is granted. Fig(s) _____
Pencil and non black ink not permitted. Fig(s) _____
2. PHOTOGRAPHS. 37 CFR 1.84(b)
One (1) full-tone set is required. Fig(s) _____
Photographs may not be mounted. 37 CFR 1.84(e)
Photographs must meet paper size requirements of 37 CFR 1.84(f). Fig(s) _____
Poor quality (half-tone). Fig(s) _____
3. TYPE OF PAPER. 37 CFR 1.84(e)
Paper not flexible, strong, white, and durable. Fig(s) _____
Erasures, alterations, overwritings, interlineations, folds, copy machine marks not accepted. Fig(s) _____
4. SIZE OF PAPER. 37 CFR 1.84(f): Acceptable sizes:
21.0 cm by 29.7 cm (DIN size A4) or
21.6 cm by 27.9 cm (8 1/2 x 11 inches)
All drawing sheets not the same size. Sheet(s) _____
Drawings sheets not an acceptable size. Fig(s) _____
5. MARGINS. 37 CFR 1.84(g): Acceptable margins:
Top 2.5 cm Left 2.5 cm Right 1.5 cm Bottom 1.0 cm
Margins not acceptable. Fig(s) _____
Top (T) _____ Left (L) _____
Right (R) _____ Bottom (B) _____
6. VIEWS. 37 CFR 1.84(h)
REMINDER: Specification may require revision to correspond to drawing changes, e.g., if Fig. 1 is changed to Fig. 1A, Fig 1B and Fig. 1C, etc., the specification, at the Brief Description of the Drawings, must likewise be changed.
Views not labeled separately or properly. Fig(s) _____
7. SECTIONAL VIEWS. 37 CFR 1.84(h)(3)
Sectional designation should be noted with Arabic or Roman numbers. Fig(s) _____

8. ARRANGEMENT OF VIEWS. 37 CFR 1.84(i)
Words do not appear on a horizontal, left-to-right fashion when page is either upright or turned so that the top becomes the right side, except for graphs. Fig(s) _____
9. SCALE. 37 CFR 1.84(k)
Scale not large enough to show mechanism without crowding when drawing is reduced in size to two-thirds in reproduction. Fig(s) _____
10. CHARACTER OF LINES, NUMBERS, & LETTERS. 37 CFR 1.84(l)
Lines, numbers & letters not uniformly thick and well defined, clean, durable, and black (poor line quality). Fig(s) _____
11. SHADING. 37 CFR 1.84(m)
Solid black areas pale. Fig(s) _____
Solid black shading not permitted. Fig(s) _____
12. NUMBERS, LETTERS, & REFERENCE CHARACTERS. 37 CFR 1.84(p)
Numbers and reference characters not plain and legible. Fig(s) _____
Figure legends are poor. Fig(s) _____
Numbers and reference characters not oriented in the same direction as the view. 37 CFR 1.84(p)(1) Fig(s) _____
English alphabet not used. 37 CFR 1.84(p)(2) Fig(s) _____
Numbers, letters and reference characters must be at least 32 cm (1/8 inch) in height. 37 CFR 1.84(p)(3). Fig(s) _____
13. LEAD LINES. 37 CFR 1.84(q)
Lead lines missing. Fig(s) _____
14. NUMBERING OF SHEETS OF DRAWINGS. 37 CFR 1.84(t)
Sheets not numbered consecutively, and in Arabic numbers beginning with number 1. Sheet(s) _____
15. NUMBERING OF VIEWS. 37 CFR 1.84(u)
Views not numbered consecutively, and in Arabic numerals, beginning with number 1. Fig(s) _____
16. DESIGN DRAWINGS. 37 CFR 1.152
Surface shading shown not appropriate. Fig(s) _____
Solid black surface shading is not permitted except when used to represent the color black as well as color contrast. Fig(s) _____

COMMENTS:

Reviewer Tang

If you have questions, call (703)

305.0333 x 132

Date 01/10/06

Attachment to Paper No. _____

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JAN 10 REC'D

Patenting Division

13

Application No. : 09/868,677
Applicant : Samuel J. Davis et al.
Filed : October 01, 2001
TC/A.U. : 1646
Examiner : O'Hara, Eileen
Docket No. : REG 670A-US
Customer No. : 26693

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Attention: Nhan Tang

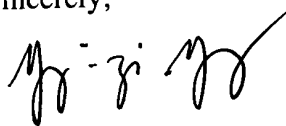
Dear Mr. Tang,

As per our conversation, I am sending you the Drawings that I have in our file for the above-mentioned application for your review. These Drawings were filed with USPTO on October 1, 2001.

Please let me know if these Drawings are acceptable. If not, please contact me at your earliest convenience.

Thank you for your attention to this matter and I look forward hearing from you soon.

Sincerely,



Ying-Zi Yang, Ph.D.
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Tarrytown, New York 10591
Tel.: (914) 345-7814

Fig.1 A.

A. 10 20 30 40 50

ATG TCT GCA CTT CTG ATC CTA GCT CTT GTT GGA GCT GCA GTT GCT
Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala>
_a_a_a_a_TRYPsin SIGNAL SEQUENCE_a_a_a_a_>

50 60 70 80 90

AGA GAC TGT GCA GAT GTA TAT CAA GCT GGT TTT AAT AAA AGT GGA
Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

100 110 120 130

ATC TAC ACT ATT TAT ATT AAT AAT ATG CCA GAA CCC AAA AAG GTG
Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

140 150 160 170 180

TTT TGC AAT ATG GAT GTC AAT GGG GGA GGT TGG ACT GTA ATA CAA
Phe Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

190 200 210 220

CAT CGT GAA GAT GGA AGT CTA GAT TTC CAA AGA GGC TGG AAG GAA
His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

230 240 250 260 270

TAT AAA ATG GGT TTT GGA AAT CCC TCC GGT GAA TAT TGG CTG GGG
Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

280 290 300 310

AAT GAG TTT ATT TTT GCC ATT ACC AGT CAG AGG CAG TAC ATG CTA
Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

320 330 340 350 360

AGA ATT GAG TTA ATG GAC TGG GAA GGG AAC CGA GCC TAT TCA CAG
Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

370 380 390 400

TAT GAC AGA TTC CAC ATA GGA AAT GAA AAG CAA AAC TAT AGG TTG
Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

410 420 430 440 450

TAT TTA AAA GGT CAC ACT GGG ACA GCA GGA AAA CAG AGC AGC CTG
Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu>
_b_b_b_b_ANG1 FIBRINOGEN-LIKE DOMAIN_b_b_b_b_>

Fig.1B.

```

      460      470      480      490
      *      *      *      *      *
ATC TTA CAC GGT GCT GAT TTC AGC ACT AAA GAT GCT GAT AAT GAC
Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      500      510      520      530      540
      *      *      *      *      *
AAC TGT ATG TGC AAA TGT GCC CTC ATG TTA ACA GGA GGA TGG TGG
Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      550      560      570      580
      *      *      *      *      *
TTT GAT GCT TGT GGC CCC TCC AAT CTA AAT GGA ATG TTC TAT ACT
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      590      600      610      620      630
      *      *      *      *      *
GCG GGA CAA AAC CAT GGA AAA CTG AAT GGG ATA AAG TGG CAC TAC
Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      640      650      660      670
      *      *      *      *      *
TTC AAA GGG CCC AGT TAC TCC TTA CGT TCC ACA ACT ATG ATG ATT
Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      680      690      700      710      720
      *      *      *      *      *
CGA CCT TTA GAT TTT GGC CCC GCG CCT TTT AGA GAC TGT GCA GAT
Arg Pro Leu Asp Phe>
__ANG1 FIBRINO__>
      Gly Pro Ala Pro>
      __GPAP BRI__>
      Phe Arg Asp Cys Ala Asp>
      __ANG1 FIBRINOGEN-__>

      730      740      750      760
      *      *      *      *      *
GTA TAT CAA GCT GGT TTT AAT AAA AGT GGA ATC TAC ACT ATT TAT
Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      770      780      790      800      810
      *      *      *      *      *
ATT AAT AAT ATG CCA GAA CCC AAA AAG GTG TTT TGC AAT ATG GAT
Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      820      830      840      850
      *      *      *      *      *
GTC AAT GGG GGA GGT TGG ACT GTA ATA CAA CAT CGT GAA GAT GGA
Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

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Fig.1C.

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      860      870      880      890      900
      *      *      *      *      *
AGT CTA GAT TTC CAA AGA GGC TGG AAG GAA TAT AAA ATG GGT TTT
Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      910      920      930      940
      *      *      *      *      *
GGA AAT CCC TCC GGT GAA TAT TGG CTG GGG AAT GAG TTT ATT TTT
Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      950      960      970      980      990
      *      *      *      *      *
GCC ATT ACC AGT CAG AGG CAG TAC ATG CTA AGA ATT GAG TTA ATG
Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      1000      1010      1020      1030
      *      *      *      *      *
GAC TGG GAA GGG AAC CGA GCC TAT TCA CAG TAT GAC AGA TTC CAC
Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      1040      1050      1060      1070      1080
      *      *      *      *      *
ATA GGA AAT GAA AAG CAA AAC TAT AGG TTG TAT TTA AAA GGT CAC
Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      1090      1100      1110      1120
      *      *      *      *      *
ACT GGG ACA GCA GGA AAA CAG AGC AGC CTG ATC TTA CAC GGT GCT
Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      1130      1140      1150      1160      1170
      *      *      *      *      *
GAT TTC AGC ACT AAA GAT GCT GAT AAT GAC AAC TGT ATG TGC AAA
Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys Lys>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      1180      1190      1200      1210
      *      *      *      *      *
TGT GCC CTC ATG TTA ACA GGA GGA TGG TGG TTT GAT GCT TGT GGC
Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      1220      1230      1240      1250      1260
      *      *      *      *      *
CCC TCC AAT CTA AAT GGA ATG TTC TAT ACT GCG GGA CAA AAC CAT
Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

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Fig.1D.

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      1270      1280      1290      1300
      *      *      *      *      *      *      *
GGA AAA CTG AAT GGG ATA AAG TGG CAC TAC TTC AAA GGG CCC AGT
Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      1310      1320      1330      1340      1350
      *      *      *      *      *      *      *
TAC TCC TTA CGT TCC ACA ACT ATG ATG ATT CGA CCT TTA GAT TTT
Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe>
__d__d__d__ANG1 FIBRINOGEN-LIKE DOMAIN_d__d__d__d__>

      1360      1370      1380      1390
      *      *      *      *      *      *      *
GGA CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA
Gly Pro Gly>
__e__e__>
      Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro>
      __f__f__f__FC TAG [SPLIT]__f__f__f__f__>

      1400      1410      1420      1430      1440
      *      *      *      *      *      *      *
CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu>
__f__f__f__f__f__FC TAG [SPLIT]__f__f__f__f__f__>

      1450      1460      1470      1480
      *      *      *      *      *      *      *
TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro>
__f__f__f__f__f__FC TAG [SPLIT]__f__f__f__f__f__>

      1490      1500      1510      1520      1530
      *      *      *      *      *      *      *
GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu>
__f__f__f__f__f__FC TAG [SPLIT]__f__f__f__f__f__>

      1540      1550      1560      1570
      *      *      *      *      *      *      *
GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala>
__f__f__f__f__f__FC TAG [SPLIT]__f__f__f__f__f__>

      1580      1590      1600      1610      1620
      *      *      *      *      *      *      *
AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val>
__f__f__f__f__f__FC TAG [SPLIT]__f__f__f__f__f__>

      1630      1640      1650      1660
      *      *      *      *      *      *      *
GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys>
__f__f__f__f__f__FC TAG [SPLIT]__f__f__f__f__f__>

```

Fig. 1 E.

1670 1680 1690 1700 1710
 * * * * * *
 GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile>
 ___f___f___f___f___f___FC TAG [SPLIT]___f___f___f___f___f___>

1720 1730 1740 1750
 * * * * * *
 GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln>
 ___f___f___f___f___f___FC TAG [SPLIT]___f___f___f___f___f___>

1760 1770 1780 1790 1800
 * * * * * *
 GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln>
 ___f___f___f___f___f___FC TAG [SPLIT]___f___f___f___f___f___>

1810 1820 1830 1840
 * * * * * *
 GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile>
 ___f___f___f___f___f___FC TAG [SPLIT]___f___f___f___f___f___>

1850 1860 1870 1880 1890
 * * * * * *
 GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys>
 ___f___f___f___f___f___FC TAG [SPLIT]___f___f___f___f___f___>

1900 1910 1920 1930
 * * * * * *
 ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr>
 ___f___f___f___f___f___FC TAG [SPLIT]___f___f___f___f___f___>

1940 1950 1960 1970 1980
 * * * * * *
 AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val>
 ___f___f___f___f___f___FC TAG [SPLIT]___f___f___f___f___f___>

1990 2000 2010 2020
 * * * * * *
 TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr>
 ___f___f___f___f___f___FC TAG [SPLIT]___f___f___f___f___f___>

2030 2040 2050
 * * * * *
 CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>
 ___f___f___f___f___f___FC TAG [SPLIT]___f___f___f___f___f___>

A. * * * * * 10 20 30 40

ATG TCT GCA CTT CTG ATC CTA GCT CTT GTT GGA GCT GCA GTT GCT
Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala>
_a_a_a_a_TRYPSIN SIGNAL SEQUENCE_a_a_a_a_>

50 60 70 80 90
* * * * *
AGA GAC TGT GCT GAA GTA TTC AAA TCA GGA CAC ACC ACA AAT GGC
Arg Asp Cys Ala Glu Val Phe Lys Ser Gly His Thr Thr Asn Gly>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

100 110 120 130
* * * * *
ATC TAC ACG TTA ACA TTC CCT AAT TCT ACA GAA GAG ATC AAG GCC
Ile Tyr Thr Leu Thr Phe Pro Asn Ser Thr Glu Glu Ile Lys Ala>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

140 150 160 170 180
* * * * *
TAC TGT GAC ATG GAA GCT GGA GGA GGC GGG TGG ACA ATT ATT CAG
Tyr Cys Asp Met Glu Ala Gly Gly Gly Gly Trp Thr Ile Ile Gln>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

190 200 210 220
* * * * *
CGA CGT GAG GAT GGC AGC GTT GAT TTT CAG AGG ACT TGG AAA GAA
Arg Arg Glu Asp Gly Ser Val Asp Phe Gln Arg Thr Trp Lys Glu>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

230 240 250 260 270
* * * * *
TAT AAA GTG GGA TTT GGT AAC CCT TCA GGA GAA TAT TGG CTG GGA
Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

280 290 300 310
* * * * *
AAT GAG TTT GTT TCG CAA CTG ACT AAT CAG CAA CGC TAT GTG CTT
Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg Tyr Val Leu>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

320 330 340 350 360
* * * * *
AAA ATA CAC CTT AAA GAC TGG GAA GGG AAT GAG GCT TAC TCA TTG
Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr Ser Leu>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

370 380 390 400
* * * * *
TAT GAA CAT TTC TAT CTC TCA AGT GAA GAA CTC AAT TAT AGG ATT
Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg Ile>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

410 420 430 440 450
* * * * *
CAC CTT AAA GGA CTT ACA GGG ACA GCC GGC AAA ATA AGC AGC ATC
His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile>
_b_b_b_ANG2 FIBRINOGEN-LIKE DOMAIN #1_b_b_b_>

Fig.2B.

```

      460      470      480      490
      *      *      *      *      *
AGC CAA CCA GGA AAT GAT TTT AGC ACA AAG GAT GGA GAC AAC GAC
Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      500      510      520      530      540
      *      *      *      *      *
AAA TGT ATT TGC AAA TGT TCA CAA ATG CTA ACA GGA GGC TGG TGG
Lys Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      550      560      570      580
      *      *      *      *      *
TTT GAT GCA TGT GGT CCT TCC AAC TTG AAC GGA ATG TAC TAT CCA
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      590      600      610      620      630
      *      *      *      *      *
CAG AGG CAG AAC ACA AAT AAG TTC AAC GGC ATT AAA TGG TAC TAC
Gln Arg Gln Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      640      650      660      670
      *      *      *      *      *
TGG AAA GGC TCA GGC TAT TCG CTC AAG GCC ACA ACC ATG ATG ATC
Trp Lys Gly Ser Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN #1__b__b__b__>

      680      690      700      710      720
      *      *      *      *      *
CGA CCA GCA GAT TTC GGG GGC CCC GCG CCT TTC AGA GAC TGT GCT
Arg Pro Ala Asp Phe>
__ANG2 FIBRINO__>
      Gly Gly Pro Ala Pro>
      __GGPAP BRIDGE__>
      Phe Arg Asp Cys Ala>
      __ANG2 FIBRINO__>

      730      740      750      760
      *      *      *      *      *
GAA GTA TTC AAA TCA GGA CAC ACC ACA AAT GGC ATC TAC ACG TTA
Glu Val Phe Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      770      780      790      800      810
      *      *      *      *      *
ACA TTC CCT AAT TCT ACA GAA GAG ATC AAG GCC TAC TGT GAC ATG
Thr Phe Pro Asn Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      820      830      840      850
      *      *      *      *      *
GAA GCT GGA GGA GGC GGG TGG ACA ATT ATT CAG CGA CGT GAG GAT
Glu Ala Gly Gly Gly Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

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Fig.2C.

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      860          870          880          890          900
      *          *          *          *          *
GGC AGC GTT GAT TTT CAG AGG ACT TGG AAA GAA TAT AAA GTG GGA
Gly Ser Val Asp Phe Gln Arg Thr Trp Lys Glu Tyr Lys Val Gly>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      910          920          930          940
      *          *          *          *          *
TTT GGT AAC CCT TCA GGA GAA TAT TGG CTG GGA AAT GAG TTT GTT
Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Val>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      950          960          970          980          990
      *          *          *          *          *
TCG CAA CTG ACT AAT CAG CAA CGC TAT GTG CTT AAA ATA CAC CTT
Ser Gln Leu Thr Asn Gln Gln Arg Tyr Val Leu Lys Ile His Leu>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      1000         1010         1020         1030
      *          *          *          *          *
AAA GAC TGG GAA GGG AAT GAG GCT TAC TCA TTG TAT GAA CAT TTC
Lys Asp Trp Glu Gly Asn Glu Ala Tyr Ser Leu Tyr Glu His Phe>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      1040         1050         1060         1070         1080
      *          *          *          *          *
TAT CTC TCA AGT GAA GAA CTC AAT TAT AGG ATT CAC CTT AAA GGA
Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg Ile His Leu Lys Gly>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      1090         1100         1110         1120
      *          *          *          *          *
CTT ACA GGG ACA GCC GGC AAA ATA AGC AGC ATC AGC CAA CCA GGA
Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile Ser Gln Pro Gly>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      1130         1140         1150         1160         1170
      *          *          *          *          *
AAT GAT TTT AGC ACA AAG GAT GGA GAC AAC GAC AAA TGT ATT TGC
Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys Cys Ile Cys>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      1180         1190         1200         1210
      *          *          *          *          *
AAA TGT TCA CAA ATG CTA ACA GGA GGC TGG TGG TTT GAT GCA TGT
Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      1220         1230         1240         1250         1260
      *          *          *          *          *
GGT CCT TCC AAC TTG AAC GGA ATG TAC TAT CCA CAG AGG CAG AAC
Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln Asn>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

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Fig.2D.

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      1270      1280      1290      1300
      *        *        *        *
ACA AAT AAG TTC AAC GGC ATT AAA TGG TAC TAC TGG AAA GGC TCA
Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      1310      1320      1330      1340      1350
      *        *        *        *        *
GGC TAT TCG CTC AAG GCC ACA ACC ATG ATG ATC CGA CCA GCA GAT
Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp>
__d__d__d__ANG2 FIBRINOGEN-LIKE DOMAIN#2__d__d__d__>

      1360      1370      1380      1390
      *        *        *        *        *
TTC GGA CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC
Phe>
__>
      Gly Pro Gly>
      __e__e__>
              Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys>
              __f__f__f__f__FC TAG__f__f__f__f__>

      1400      1410      1420      1430      1440
      *        *        *        *        *
CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe>
__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__>

      1450      1460      1470      1480
      *        *        *        *        *
CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr>
__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__>

      1490      1500      1510      1520      1530
      *        *        *        *        *
CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro>
__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__>

      1540      1550      1560      1570
      *        *        *        *        *
GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn>
__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__>

      1580      1590      1600      1610      1620
      *        *        *        *        *
GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg>
__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__>

      1630      1640      1650      1660
      *        *        *        *        *
GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly>
__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__>

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1670 1680 1690 1700 1710
* * * * * * * *
AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro>
__f__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__f__>

1720 1730 1740 1750
* * * * * * * *
ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro>
__f__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__f__>

1760 1770 1780 1790 1800
* * * * * * * *
CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn>
__f__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__f__>

1810 1820 1830 1840
* * * * * * * *
CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp>
__f__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__f__>

1850 1860 1870 1880 1890
* * * * * * * *
ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr>
__f__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__f__>

1900 1910 1920 1930
* * * * * * * *
AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu>
__f__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__f__>

1940 1950 1960 1970 1980
* * * * * * * *
TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn>
__f__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__f__>

1990 2000 2010 2020
* * * * * * * *
GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr>
__f__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__f__>

2030 2040 2050 2060
* * * * * * * *
ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>
__f__f__f__f__f__f__f__FC TAG__f__f__f__f__f__f__f__>

Fig.3A.

* 10 20 30 40
 * * * * *
 ATG TCT GCA CTT CTG ATC CTA GCT CTT GTT GGA GCT GCA GTT GCT
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala>
 ____a____a____a____a_TRYPSIN SIGNAL SEQUENCE____a____a____a____a____>

50 60 70 80 90
 * * * * * * *
 AGA GAC TGT GCA GAT GTA TAT CAA GCT GGT TTT AAT AAA AGT GGA
 Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly>
 ____b____b____b____ANG1 FIBRINOGEN-LIKE DOMAIN_b____b____b____b____>

100 110 120 130
 * * * * * * *
 ATC TAC ACT ATT TAT ATT AAT AAT ATG CCA GAA CCC AAA AAG GTG
 Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val>
 ____b____b____b____ANG1 FIBRINOGEN-LIKE DOMAIN_b____b____b____b____>

140 150 160 170 180
 * * * * * * *
 TTT TGC AAT ATG GAT GTC AAT GGG GGA GGT TGG ACT GTA ATA CAA
 Phe Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln>
 ____b____b____b____ANG1 FIBRINOGEN-LIKE DOMAIN_b____b____b____b____>

190 200 210 220
 * * * * * * *
 CAT CGT GAA GAT GGA AGT CTA GAT TTC CAA AGA GGC TGG AAG GAA
 His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu>
 ____b____b____b____ANG1 FIBRINOGEN-LIKE DOMAIN_b____b____b____b____>

230 240 250 260 270
 * * * * * * *
 TAT AAA ATG GGT TTT GGA AAT CCC TCC GGT GAA TAT TGG CTG GGG
 Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly>
 ____b____b____b____ANG1 FIBRINOGEN-LIKE DOMAIN_b____b____b____b____>

280 290 300 310
 * * * * * * *
 AAT GAG TTT ATT TTT GCC ATT ACC AGT CAG AGG CAG TAC ATG CTA
 Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu>
 ____b____b____b____ANG1 FIBRINOGEN-LIKE DOMAIN_b____b____b____b____>

320 330 340 350 360
 * * * * * * *
 AGA ATT GAG TTA ATG GAC TGG GAA GGG AAC CGA GCC TAT TCA CAG
 Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln>
 ____b____b____b____ANG1 FIBRINOGEN-LIKE DOMAIN_b____b____b____b____>

370 380 390 400
 * * * * * * *
 TAT GAC AGA TTC CAC ATA GGA AAT GAA AAG CAA AAC TAT AGG TTG
 Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu>
 ____b____b____b____ANG1 FIBRINOGEN-LIKE DOMAIN_b____b____b____b____>

Fig.3B.

```

      410      420      430      440      450
      *      *      *      *      *
TAT TTA AAA GGT CAC ACT GGG ACA GCA GGA AAA CAG AGC AGC CTG
Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      460      470      480      490
      *      *      *      *      *
ATC TTA CAC GGT GCT GAT TTC AGC ACT AAA GAT GCT GAT AAT GAC
Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      500      510      520      530      540
      *      *      *      *      *
AAC TGT ATG TGC AAA TGT GCC CTC ATG TTA ACA GGA GGA TGG TGG
Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      550      560      570      580
      *      *      *      *      *
TTT GAT GCT TGT GGC CCC TCC AAT CTA AAT GGA ATG TTC TAT ACT
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      590      600      610      620      630
      *      *      *      *      *
GCG GGA CAA AAC CAT GGA AAA CTG AAT GGG ATA AAG TGG CAC TAC
Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      640      650      660      670
      *      *      *      *      *
TTC AAA GGG CCA AGT TAC TCC TTA CGT TCC ACA ACT ATG ATG ATT
Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile>
__b__b__b__ANG1 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      680      690      700      710      720
      *      *      *      *      *
CGA CCT TTA GAT TTT GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA
Arg Pro Leu Asp Phe>
__ANG1 FIBRINO__>
      Gly Pro Gly>
      __c__c__>
      Glu Pro Lys Ser Cys Asp Lys>
      __d__d__FC TAG__d__d__>

      730      740      750      760
      *      *      *      *      *
ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly>
__d__d__d__d__d__d__FC TAG__d__d__d__d__d__d__>

      770      780      790      800      810
      *      *      *      *      *
CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met>
__d__d__d__d__d__d__FC TAG__d__d__d__d__d__d__>

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Fig.3C.

```

      820      830      840      850
      *      *      *      *      *
ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

      860      870      880      890      900
      *      *      *      *      *
CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

      910      920      930      940
      *      *      *      *      *
GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

      950      960      970      980      990
      *      *      *      *      *
AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

      1000      1010      1020      1030
      *      *      *      *      *
TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

      1040      1050      1060      1070      1080
      *      *      *      *      *
CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

      1090      1100      1110      1120
      *      *      *      *      *
CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

      1130      1140      1150      1160      1170
      *      *      *      *      *
CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

      1180      1190      1200      1210
      *      *      *      *      *
TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

      1220      1230      1240      1250      1260
      *      *      *      *      *
GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

```

1270 1280 1290 1300
* * * * *
TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1310 1320 1330 1340 1350
* * * * *
CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1360 1370 1380 1390
* * * * *
CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1400 1410 1420 1430 1440
* * * * *
GGC GGT GGC GGT TCT GGC GCG CCT TTT AGA GAC TGT GCA GAT GTA
Gly Gly Gly Gly Ser Gly Ala Pro>
_G4S LINKER/ASC BRIDGE (N____>
Phe Arg Asp Cys Ala Asp Val>
_ANG1 FIBRINOGEN-LIKE____>

1450 1460 1470 1480
* * * * *
TAT CAA GCT GGT TTT AAT AAA AGT GGA ATC TAC ACT ATT TAT ATT
Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile>
_f_f_f_f_ANG1 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_>

1490 1500 1510 1520 1530
* * * * *
AAT AAT ATG CCA GAA CCC AAA AAG GTG TTT TGC AAT ATG GAT GTC
Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val>
_f_f_f_f_ANG1 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_>

1540 1550 1560 1570
* * * * *
AAT GGG GGA GGT TGG ACT GTA ATA CAA CAT CGT GAA GAT GGA AGT
Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser>
_f_f_f_f_ANG1 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_>

1580 1590 1600 1610 1620
* * * * *
CTA GAT TTC CAA AGA GGC TGG AAG GAA TAT AAA ATG GGT TTT GGA
Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly>
_f_f_f_f_ANG1 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_>

1630 1640 1650 1660
* * * * *
AAT CCC TCC GGT GAA TAT TGG CTG GGG AAT GAG TTT ATT TTT GCC
Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala>
_f_f_f_f_ANG1 FIBRINOGEN-LIKE DOMAIN_f_f_f_f_f_>

Fig.3E.

```

1670      1680      1690      1700      1710
*          *          *          *          *
ATT ACC AGT CAG AGG CAG TAC ATG CTA AGA ATT GAG TTA ATG GAC
Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1720      1730      1740      1750
*          *          *          *          *
TGG GAA GGG AAC CGA GCC TAT TCA CAG TAT GAC AGA TTC CAC ATA
Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1760      1770      1780      1790      1800
*          *          *          *          *
GGA AAT GAA AAG CAA AAC TAT AGG TTG TAT TTA AAA GGT CAC ACT
Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1810      1820      1830      1840
*          *          *          *          *
GGG ACA GCA GGA AAA CAG AGC AGC CTG ATC TTA CAC GGT GCT GAT
Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1850      1860      1870      1880      1890
*          *          *          *          *
TTC AGC ACT AAA GAT GCT GAT AAT GAC AAC TGT ATG TGC AAA TGT
Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys Lys Cys>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1900      1910      1920      1930
*          *          *          *          *
GCC CTC ATG TTA ACA GGA GGA TGG TGG TTT GAT GCT TGT GGC CCC
Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly Pro>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1940      1950      1960      1970      1980
*          *          *          *          *
TCC AAT CTA AAT GGA ATG TTC TAT ACT GCG GGA CAA AAC CAT GGA
Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1990      2000      2010      2020
*          *          *          *          *
AAA CTG AAT GGG ATA AAG TGG CAC TAC TTC AAA GGG CCA AGT TAC
Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

2030      2040      2050      2060
*          *          *          *          *
TCC TTA CGT TCC ACA ACT ATG ATG ATT CGA CCT TTA GAT TTT
Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe>
__f__f__f__ANG1 FIBRINOGEN-LIKE DOMAIN__f__f__f__>

```

```

      10      20      30      40
  *      *      *      *      *
ATG TCT GCA CTT CTG ATC CTA GCT CTT GTT GGA GCT GCA GTT GCT
Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala>
__a__a__a__a__TRYPSIN SIGNAL SEQUENCE__a__a__a__a__>

      50      60      70      80      90
  *      *      *      *      *
AGA GAC TGT GCT GAA GTA TTC AAA TCA GGA CAC ACC ACA AAT GGC
Arg Asp Cys Ala Glu Val Phe Lys Ser Gly His Thr Thr Asn Gly>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      100      110      120      130
  *      *      *      *      *
ATC TAC ACG TTA ACA TTC CCT AAT TCT ACA GAA GAG ATC AAG GCC
Ile Tyr Thr Leu Thr Phe Pro Asn Ser Thr Glu Glu Ile Lys Ala>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      140      150      160      170      180
  *      *      *      *      *
TAC TGT GAC ATG GAA GCT GGA GGA GGC GGG TGG ACA ATT ATT CAG
Tyr Cys Asp Met Glu Ala Gly Gly Gly Gly Trp Thr Ile Ile Gln>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      190      200      210      220
  *      *      *      *      *
CGA CGT GAG GAT GGC AGC GTT GAT TTT CAG AGG ACT TGG AAA GAA
Arg Arg Glu Asp Gly Ser Val Asp Phe Gln Arg Thr Trp Lys Glu>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      230      240      250      260      270
  *      *      *      *      *
TAT AAA GTG GGA TTT GGT AAC CCT TCA GGA GAA TAT TGG CTG GGA
Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      280      290      300      310
  *      *      *      *      *
AAT GAG TTT GTT TCG CAA CTG ACT AAT CAG CAA CGC TAT GTG CTT
Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg Tyr Val Leu>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      320      330      340      350      360
  *      *      *      *      *
AAA ATA CAC CTT AAA GAC TGG GAA GGG AAT GAG GCT TAC TCA TTG
Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr Ser Leu>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

      370      380      390      400
  *      *      *      *      *
TAT GAA CAT TTC TAT CTC TCA AGT GAA GAA CTC AAT TAT AGG ATT
Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg Ile>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN__b__b__b__b__>

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Fig.4B.

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      410      420      430      440      450
      *      *      *      *      *
CAC CTT AAA GGA CTT ACA GGG ACA GCC GGC AAA ATA AGC AGC ATC
His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      460      470      480      490
      *      *      *      *      *
AGC CAA CCA GGA AAT GAT TTT AGC ACA AAG GAT GGA GAC AAC GAC
Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      500      510      520      530      540
      *      *      *      *      *
AAA TGT ATT TGC AAA TGT TCA CAA ATG CTA ACA GGA GGC TGG TGG
Lys Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      550      560      570      580
      *      *      *      *      *
TTT GAT GCA TGT GGT CCT TCC AAC TTG AAC GGA ATG TAC TAT CCA
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      590      600      610      620      630
      *      *      *      *      *
CAG AGG CAG AAC ACA AAT AAG TTC AAC GGC ATT AAA TGG TAC TAC
Gln Arg Gln Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      640      650      660      670
      *      *      *      *      *
TGG AAA GGC TCA GGC TAT TCG CTC AAG GCC ACA ACC ATG ATG ATC
Trp Lys Gly Ser Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile>
__b__b__b__ANG2 FIBRINOGEN-LIKE DOMAIN_b__b__b__b__>

      680      690      700      710      720
      *      *      *      *      *
CGA CCA GCA GAT TTC GGG GGC CCG GGC GAG CCC AAA TCT TGT GAC
Arg Pro Ala Asp Phe>
__ANG2 FIBRINO__>
      Gly Gly Pro Gly>
      __GGPG BRI__>
      Glu Pro Lys Ser Cys Asp>
      __d__FC TAG_d__d__>

      730      740      750      760
      *      *      *      *      *
AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly>
__d__d__d__d__d__d__FC TAG__d__d__d__d__d__d__>

      770      780      790      800      810
      *      *      *      *      *
GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu>
__d__d__d__d__d__d__FC TAG__d__d__d__d__d__d__>

```

4C. * 820 * 830 * 840 * 850 *

ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

860 870 880 890 900
* * * * *
AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

910 920 930 940
* * * * *
GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

950 960 970 980 990
* * * * *
AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1000 1010 1020 1030
* * * * *
GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1040 1050 1060 1070 1080
* * * * *
GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1090 1100 1110 1120
* * * * *
CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1130 1140 1150 1160 1170
* * * * *
GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1180 1190 1200 1210
* * * * *
TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

1220 1230 1240 1250 1260
* * * * *
CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp>
_d_d_d_d_d_d_d_FC TAG_d_d_d_d_d_d_d_d>

D. * * * * *

GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg>
__d__d__d__d__d__d__d__FC TAG__d__d__d__d__d__d__>

1310 1320 1330 1340 1350
* * * * *
TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala>
__d__d__d__d__d__d__d__FC TAG__d__d__d__d__d__d__>

1360 1370 1380 1390
* * * * *
CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly>
__d__d__d__d__d__d__d__FC TAG__d__d__d__d__d__d__>

1400 1410 1420 1430 1440
* * * * *
AAA GGC GGT GGC GGT TCT GGC GCG CCT AGA GAC TGT GCT GAA GTA
Lys>

Gly Gly Gly Gly Ser Gly Ala Pro>
__e__GGGGSGAP BRIDGE_e__e__>

Arg Asp Cys Ala Glu Val>
__ANG2 FIBRINOGEN-____>

1450 1460 1470 1480
* * * * *
TTC AAA TCA GGA CAC ACC ACA AAT GGC ATC TAC ACG TTA ACA TTC
Phe Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe>
__f__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1490 1500 1510 1520 1530
* * * * *
CCT AAT TCT ACA GAA GAG ATC AAG GCC TAC TGT GAC ATG GAA GCT
Pro Asn Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala>
__f__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1540 1550 1560 1570
* * * * *
GGA GGA GGC GGG TGG ACA ATT ATT CAG CGA CGT GAG GAT GGC AGC
Gly Gly Gly Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser>
__f__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1580 1590 1600 1610 1620
* * * * *
GTT GAT TTT CAG AGG ACT TGG AAA GAA TAT AAA GTG GGA TTT GGT
Val Asp Phe Gln Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly>
__f__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1630 1640 1650 1660
* * * * *
AAC CCT TCA GGA GAA TAT TGG CTG GGA AAT GAG TTT GTT TCG CAA
Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln>
__f__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

Fig.4E.

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1670      1680      1690      1700      1710
  *        *        *        *        *
CTG ACT AAT CAG CAA CGC TAT GTG CTT AAA ATA CAC CTT AAA GAC
Leu Thr Asn Gln Gln Arg Tyr Val Leu Lys Ile His Leu Lys Asp>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1720      1730      1740      1750
  *        *        *        *        *
TGG GAA GGG AAT GAG GCT TAC TCA TTG TAT GAA CAT TTC TAT CTC
Trp Glu Gly Asn Glu Ala Tyr Ser Leu Tyr Glu His Phe Tyr Leu>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1760      1770      1780      1790      1800
  *        *        *        *        *
TCA AGT GAA GAA CTC AAT TAT AGG ATT CAC CTT AAA GGA CTT ACA
Ser Ser Glu Glu Leu Asn Tyr Arg Ile His Leu Lys Gly Leu Thr>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1810      1820      1830      1840
  *        *        *        *        *
GGG ACA GCC GGC AAA ATA AGC AGC ATC AGC CAA CCA GGA AAT GAT
Gly Thr Ala Gly Lys Ile Ser Ser Ile Ser Gln Pro Gly Asn Asp>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1850      1860      1870      1880      1890
  *        *        *        *        *
TTT AGC ACA AAG GAT GGA GAC AAC GAC AAA TGT ATT TGC AAA TGT
Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys Cys Ile Cys Lys Cys>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1900      1910      1920      1930
  *        *        *        *        *
TCA CAA ATG CTA ACA GGA GGC TGG TGG TTT GAT GCA TGT GGT CCT
Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly Pro>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

1940      1950      1960      1970      1980
  *        *        *        *        *
TCC AAC TTG AAC GGA ATG TAC TAT CCA CAG AGG CAG AAC ACA AAT
Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln Asn Thr Asn>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

      1990      2000      2010      2020
  *        *        *        *        *
AAG TTC AAC GGC ATT AAA TGG TAC TAC TGG AAA GGC TCA GGC TAT
Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser Gly Tyr>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN_f__f__f__f__>

2030      2040      2050      2060      2070
  *        *        *        *        *
TCG CTC AAG GCC ACA ACC ATG ATG ATC CGA CCA GCA GAT TTC TGA
Ser Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp Phe>
__f__f__f__ANG2 FIBRINOGEN-LIKE DOMAIN__f__f__f__f__>

```

Fig.5.

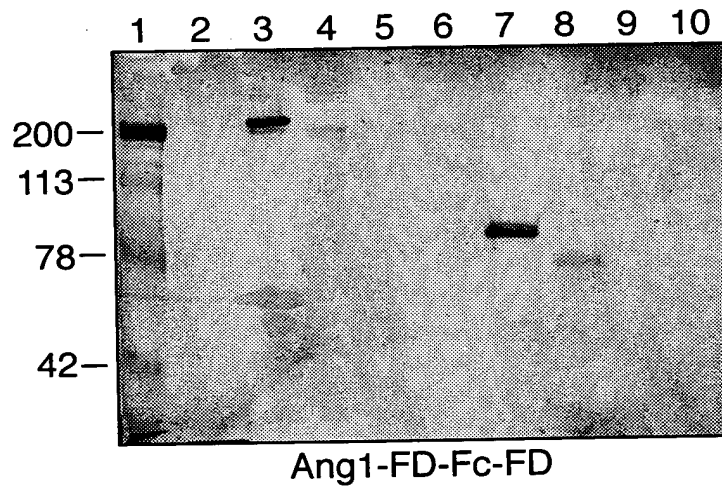


Fig.7.

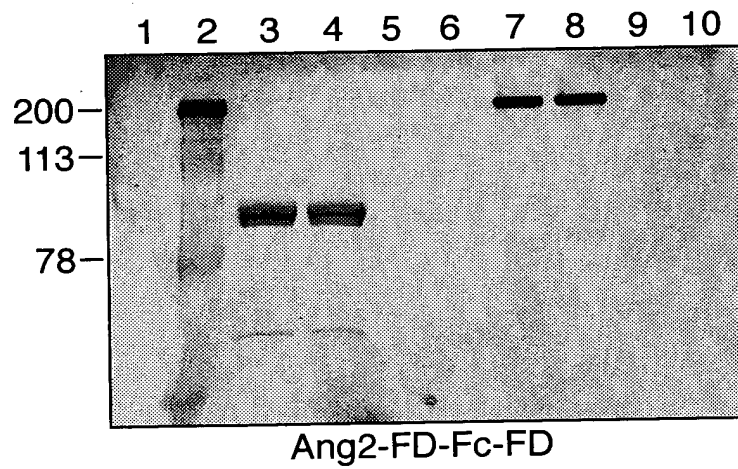


Fig.6.

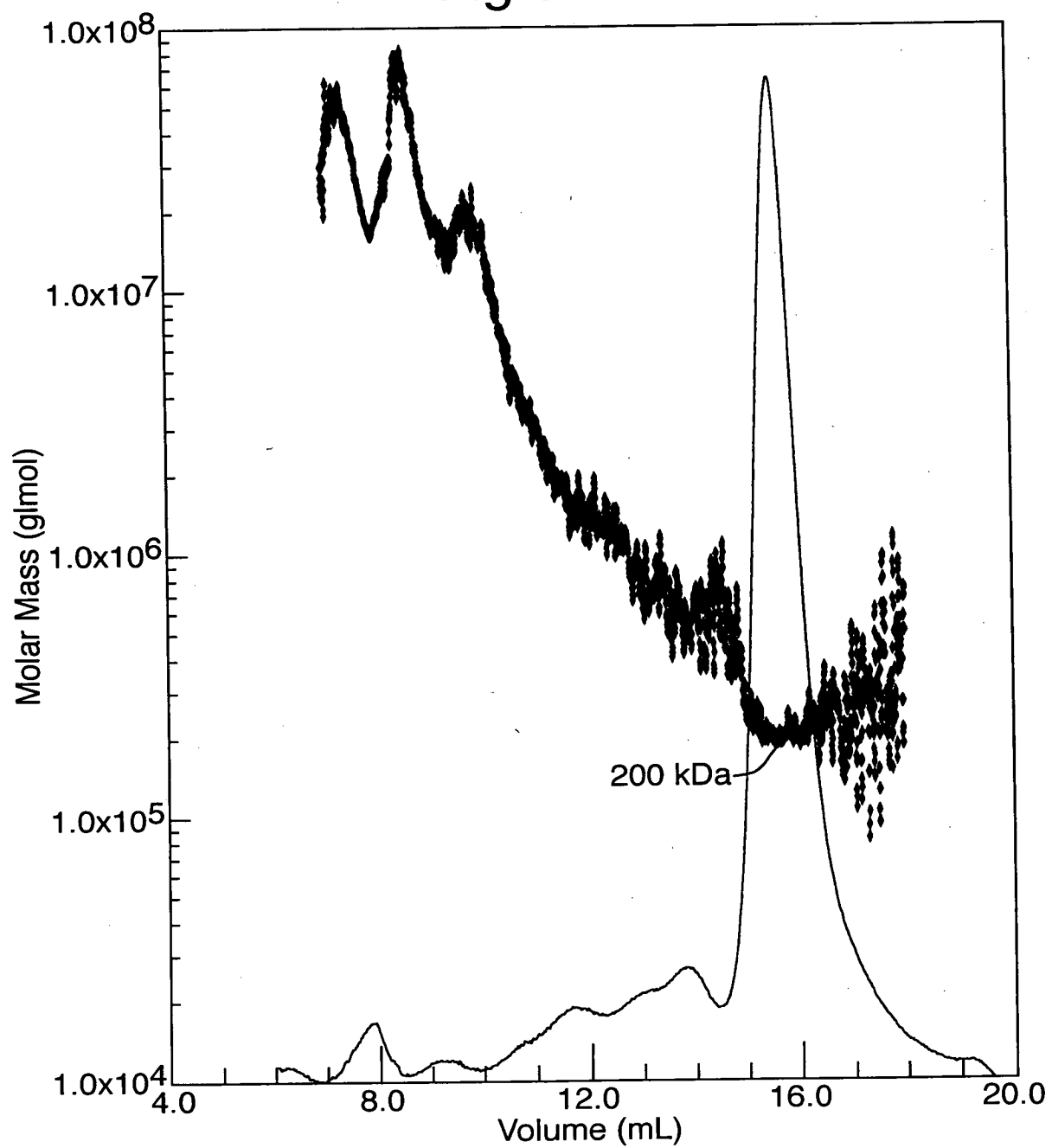


Fig.8.

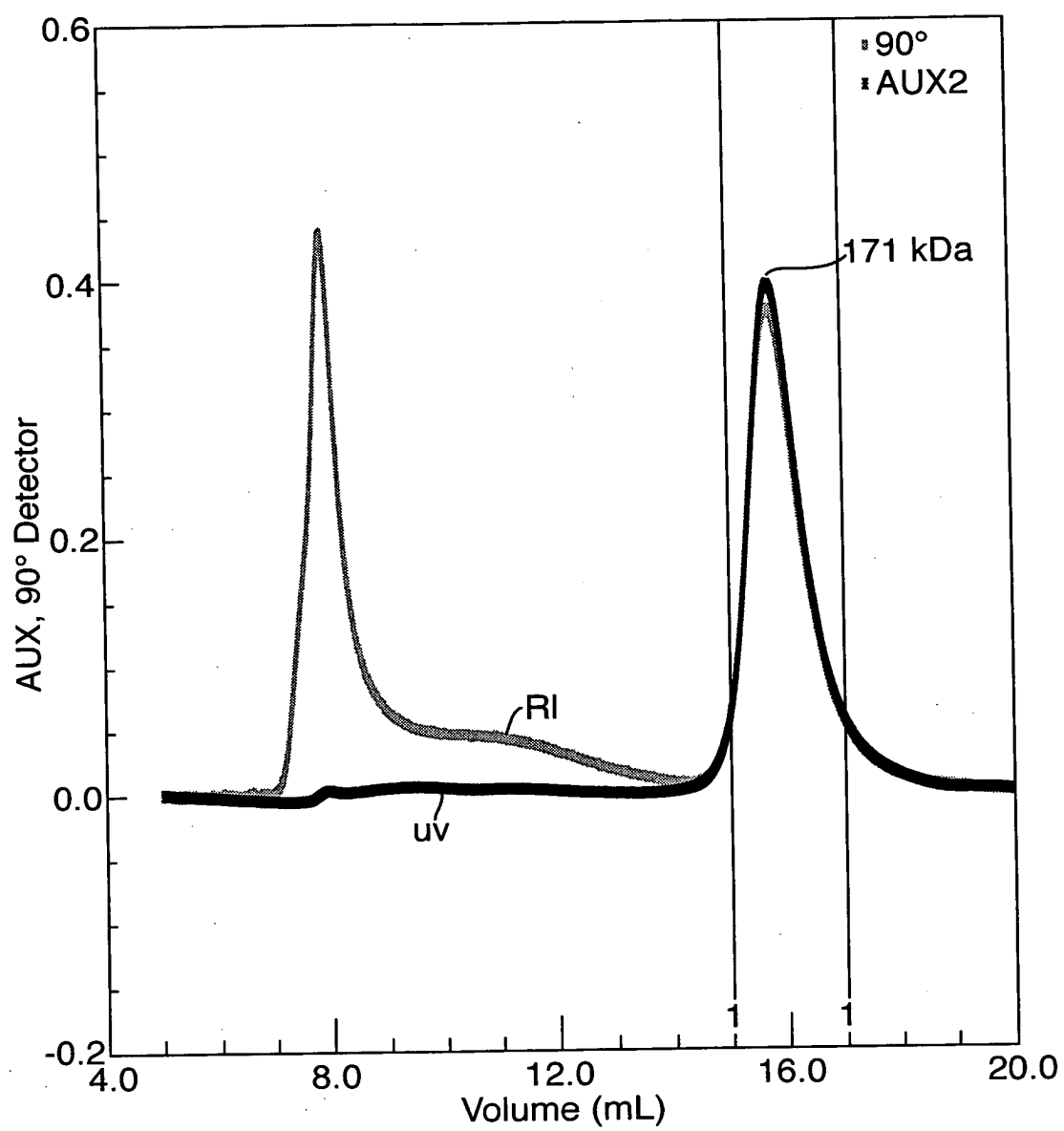


Fig.9.

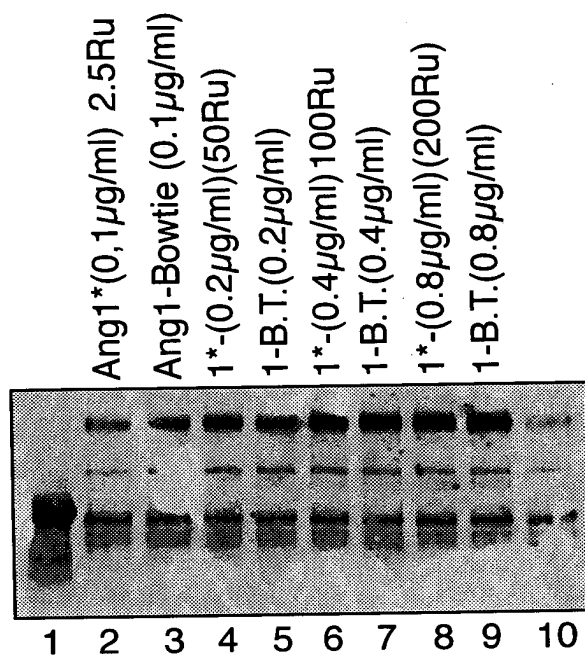


Fig.10.

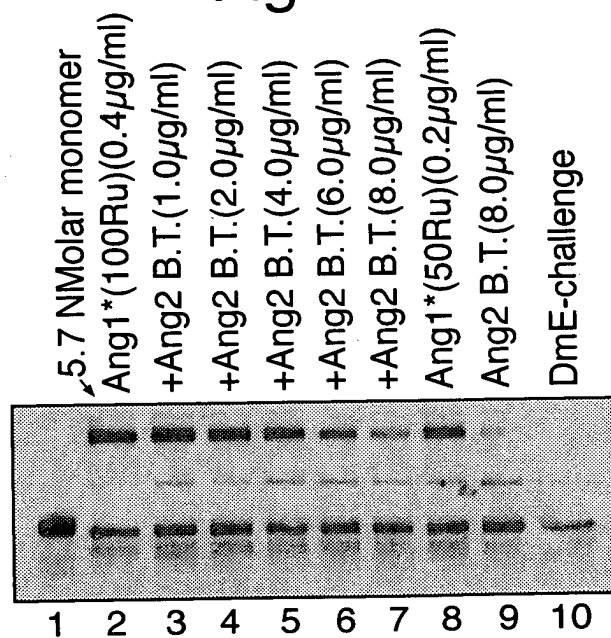


Fig.11.

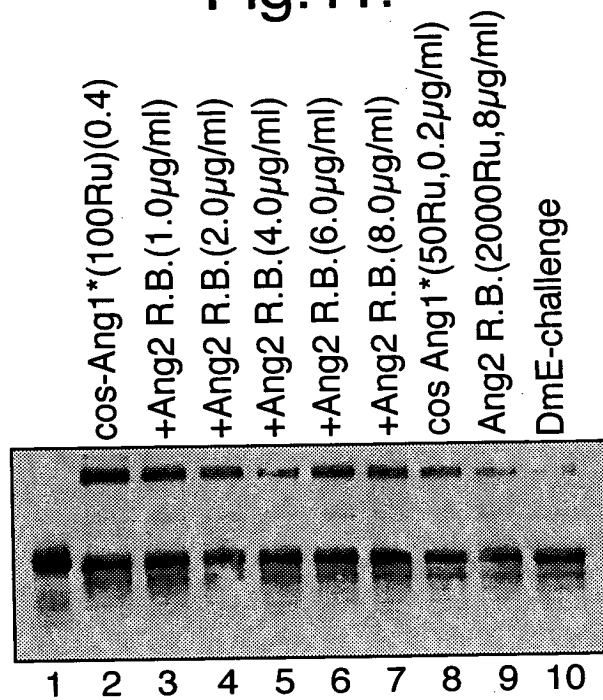


Fig.12.

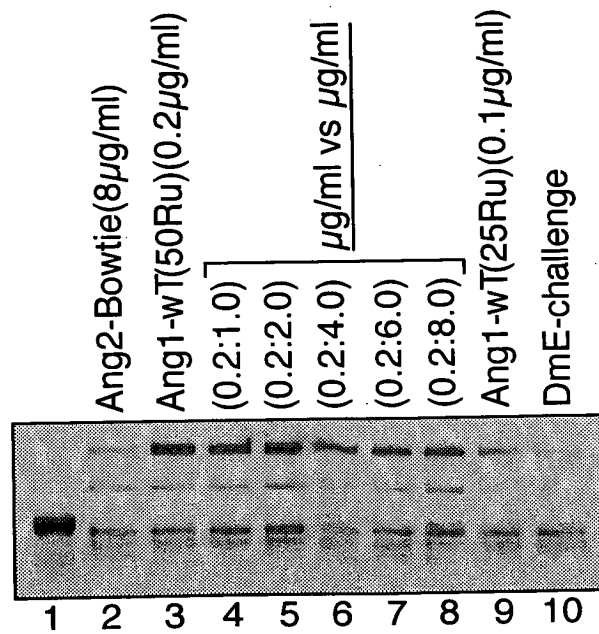


Fig.13.

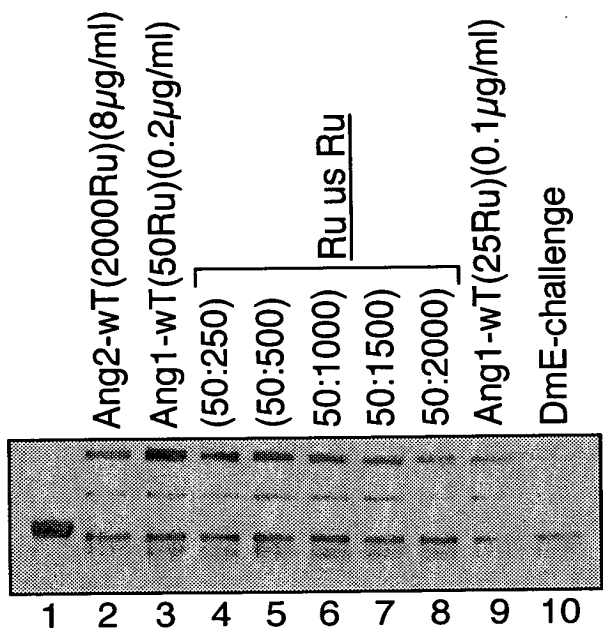


Fig.14A.

```

      10      20      30      40
      *      *      *      *      *
ATG GCT CGG CCT GGG CAG CGT TGG CTC GGC AAG TGG CTT GTG GCG
Met Ala Arg Pro Gly Gln Arg Trp Leu Gly Lys Trp Leu Val Ala>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

      50      60      70      80      90
      *      *      *      *      *
ATG GTC GTG TGG GCG CTG TGC CGG CTC GCC ACA CCG CTG GCC AAG
Met Val Val Trp Ala Leu Cys Arg Leu Ala Thr Pro Leu Ala Lys>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     100     110     120     130
      *      *      *      *      *
AAC CTG GAG CCC GTA TCC TGG AGC TCC CTC AAC CCC AAG TTC CTG
Asn Leu Glu Pro Val Ser Trp Ser Ser Leu Asn Pro Lys Phe Leu>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     140     150     160     170     180
      *      *      *      *      *
AGT GGG AAG GGC TTG GTG ATC TAT CCG AAA ATT GGA GAC AAG CTG
Ser Gly Lys Gly Leu Val Ile Tyr Pro Lys Ile Gly Asp Lys Leu>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     190     200     210     220
      *      *      *      *      *
GAC ATC ATC TGC CCC CGA GCA GAA GCA GGG CGG CCC TAT GAG TAC
Asp Ile Ile Cys Pro Arg Ala Glu Ala Gly Arg Pro Tyr Glu Tyr>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     230     240     250     260     270
      *      *      *      *      *
TAC AAG CTG TAC CTG GTG CGG CCT GAG CAG GCA GCT GCC TGT AGC
Tyr Lys Leu Tyr Leu Val Arg Pro Glu Gln Ala Ala Ala Cys Ser>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     280     290     300     310
      *      *      *      *      *
ACA GTT CTC GAC CCC AAC GTG TTG GTC ACC TGC AAT AGG CCA GAG
Thr Val Leu Asp Pro Asn Val Leu Val Thr Cys Asn Arg Pro Glu>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     320     330     340     350     360
      *      *      *      *      *
CAG GAA ATA CGC TTT ACC ATC AAG TTC CAG GAG TTC AGC CCC AAC
Gln Glu Ile Arg Phe Thr Ile Lys Phe Gln Glu Phe Ser Pro Asn>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

     370     380     390     400
      *      *      *      *      *
TAC ATG GGC CTG GAG TTC AAG AAG CAC CAT GAT TAC TAC ATT ACC
Tyr Met Gly Leu Glu Phe Lys Lys His His Asp Tyr Tyr Ile Thr>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

```

Fig.14B.

```

410          420          430          440          450
*           *           *           *           *
TCA ACA TCC AAT GGA AGC CTG GAG GGG CTG GAA AAC CGG GAG GGC
Ser Thr Ser Asn Gly Ser Leu Glu Gly Leu Glu Asn Arg Glu Gly>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

          460          470          480          490
*           *           *           *           *
GGT GTG TGC CGC ACA CGC ACC ATG AAG ATC ATC ATG AAG GTT GGG
Gly Val Cys Arg Thr Arg Thr Met Lys Ile Ile Met Lys Val Gly>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

          500          510          520          530          540
*           *           *           *           *
CAA GAT CCC AAT GCT GTG ACG CCT GAG CAG CTG ACT ACC AGC AGG
Gln Asp Pro Asn Ala Val Thr Pro Glu Gln Leu Thr Thr Ser Arg>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

          550          560          570          580
*           *           *           *           *
CCC AGC AAG GAG GCA GAC AAC ACT GTC AAG ATG GCC ACA CAG GCC
Pro Ser Lys Glu Ala Asp Asn Thr Val Lys Met Ala Thr Gln Ala>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

          590          600          610          620          630
*           *           *           *           *
CCT GGT AGT CGG GGC TCC CTG GGT GAC TCT GAT GGC AAG CAT GAG
Pro Gly Ser Arg Gly Ser Leu Gly Asp Ser Asp Gly Lys His Glu>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

          640          650          660          670
*           *           *           *           *
ACT GTG AAC CAG GAA GAG AAG AGT GGC CCA GGT GCA AGT GGG GGC
Thr Val Asn Gln Glu Glu Lys Ser Gly Pro Gly Ala Ser Gly Gly>
__a__a__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)__a__a__>

          680          690          700          710          720
*           *           *           *           *
AGC AGC GGG GAC CCT GAT GGC TTC TTC AAC TCC AAG GGC CCG GGT
Ser Ser Gly Asp Pro Asp Gly Phe Phe Asn Ser Lys>
__ELK-L ECTODOMAIN 1 (WITH SIGNAL PEPTIDE)____>
Gly Pro Gly>
__b__b__>

          730          740          750          760
*           *           *           *           *
AAG AAC CTG GAG CCC GTA TCC TGG AGC TCC CTC AAC CCC AAG TTC
Lys Asn Leu Glu Pro Val Ser Trp Ser Ser Leu Asn Pro Lys Phe>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

          770          780          790          800          810
*           *           *           *           *
CTG AGT GGG AAG GGC TTG GTG ATC TAT CCG AAA ATT GGA GAC AAG
Leu Ser Gly Lys Gly Leu Val Ile Tyr Pro Lys Ile Gly Asp Lys>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

```

Fig.14C.

```

      820      830      840      850
      *      *      *      *
CTG GAC ATC ATC TGC CCC CGA GCA GAA GCA GGG CGG CCC TAT GAG
Leu Asp Ile Ile Cys Pro Arg Ala Glu Ala Gly Arg Pro Tyr Glu>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

      860      870      880      890      900
      *      *      *      *      *
TAC TAC AAG CTG TAC CTG GTG CGG CCT GAG CAG GCA GCT GCC TGT
Tyr Tyr Lys Leu Tyr Leu Val Arg Pro Glu Gln Ala Ala Ala Cys>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

      910      920      930      940
      *      *      *      *      *
AGC ACA GTT CTC GAC CCC AAC GTG TTG GTC ACC TGC AAT AGG CCA
Ser Thr Val Leu Asp Pro Asn Val Leu Val Thr Cys Asn Arg Pro>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

      950      960      970      980      990
      *      *      *      *      *
GAG CAG GAA ATA CGC TTT ACC ATC AAG TTC CAG GAG TTC AGC CCC
Glu Gln Glu Ile Arg Phe Thr Ile Lys Phe Gln Glu Phe Ser Pro>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

     1000     1010     1020     1030
      *      *      *      *      *
AAC TAC ATG GGC CTG GAG TTC AAG AAG CAC CAT GAT TAC TAC ATT
Asn Tyr Met Gly Leu Glu Phe Lys Lys His His Asp Tyr Tyr Ile>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

     1040     1050     1060     1070     1080
      *      *      *      *      *
ACC TCA ACA TCC AAT GGA AGC CTG GAG GGG CTG GAA AAC CGG GAG
Thr Ser Thr Ser Asn Gly Ser Leu Glu Gly Leu Glu Asn Arg Glu>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

     1090     1100     1110     1120
      *      *      *      *      *
GGC GGT GTG TGC CGC ACA CGC ACC ATG AAG ATC ATC ATG AAG GTT
Gly Gly Val Cys Arg Thr Arg Thr Met Lys Ile Ile Met Lys Val>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

     1130     1140     1150     1160     1170
      *      *      *      *      *
GGG CAA GAT CCC AAT GCT GTG ACG CCT GAG CAG CTG ACT ACC AGC
Gly Gln Asp Pro Asn Ala Val Thr Pro Glu Gln Leu Thr Thr Ser>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

     1180     1190     1200     1210
      *      *      *      *      *
AGG CCC AGC AAG GAG GCA GAC AAC ACT GTC AAG ATG GCC ACA CAG
Arg Pro Ser Lys Glu Ala Asp Asn Thr Val Lys Met Ala Thr Gln>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

     1220     1230     1240     1250     1260
      *      *      *      *      *
GCC CCT GGT AGT CGG GGC TCC CTG GGT GAC TCT GAT GGC AAG CAT
Ala Pro Gly Ser Arg Gly Ser Leu Gly Asp Ser Asp Gly Lys His>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

```

Fig.14D.

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      1270      1280      1290      1300
      *      *      *      *      *      *      *      *
GAG ACT GTG AAC CAG GAA GAG AAG AGT GGC CCA GGT GCA AGT GGG
Glu Thr Val Asn Gln Glu Glu Lys Ser Gly Pro Gly Ala Ser Gly>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>

      1310      1320      1330      1340      1350
      *      *      *      *      *      *      *      *
GGC AGC AGC GGG GAC CCT GAT GGC TTC TTC AAC TCC AAA GGC CCG
Gly Ser Ser Gly Asp Pro Asp Gly Phe Phe Asn Ser Lys>
__c__c__c__ELK-L ECTODOMAIN 2 (NO SIGNAL)__c__c__c__>
                                     Gly Pro>
                                     __d__>

      1360      1370      1380      1390
      *      *      *      *      *      *      *      *
GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC
Gly>
__>
      Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys>
      __e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1400      1410      1420      1430      1440
      *      *      *      *      *      *      *      *
CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1450      1460      1470      1480
      *      *      *      *      *      *      *      *
CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1490      1500      1510      1520      1530
      *      *      *      *      *      *      *      *
ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1540      1550      1560      1570
      *      *      *      *      *      *      *      *
TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1580      1590      1600      1610      1620
      *      *      *      *      *      *      *      *
AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

      1630      1640      1650      1660
      *      *      *      *      *      *      *      *
GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr>
__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__>

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Fig.14E.

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1670      1680      1690      1700      1710
  *      *      *      *      *
AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys>
__e__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__e__>

      1720      1730      1740      1750
  *      *      *      *      *
ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr>
__e__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__e__>

1760      1770      1780      1790      1800
  *      *      *      *      *
ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser>
__e__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__e__>

      1810      1820      1830      1840
  *      *      *      *      *
CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val>
__e__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__e__>

1850      1860      1870      1880      1890
  *      *      *      *      *
GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr>
__e__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__e__>

      1900      1910      1920      1930
  *      *      *      *      *
CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys>
__e__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__e__>

1940      1950      1960      1970      1980
  *      *      *      *      *
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser>
__e__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__e__>

      1990      2000      2010      2020
  *      *      *      *      *
TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys>
__e__e__e__e__e__HUMAN IGG1 FC TAG__e__e__e__e__e__>

2030      2040      2050
  *      *      *      *      *
AGC CTC TCC CTG TCT CCG GGT AAA TGA
Ser Leu Ser Leu Ser Pro Gly Lys ***>
__e__HUMAN IGG1 FC TAG__e__e__e__>

```

Fig.15A.

```

      10      20      30      40
      *      *      *      *      *
ATG GCC ATG GCC CGG TCC AGG AGG GAC TCT GTG TGG AAG TAC TGT
Met Ala Met Ala Arg Ser Arg Arg Asp Ser Val Trp Lys Tyr Cys>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

      50      60      70      80      90
      *      *      *      *      *
TGG GGA CTT TTG ATG GTT TTG TGC AGA ACT GCG ATC TCC AGA TCG
Trp Gly Leu Leu Met Val Leu Cys Arg Thr Ala Ile Ser Arg Ser>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

     100     110     120     130
      *      *      *      *      *
ATA GTT TTA GAG CCT ATC TAC TGG AAT TCC TCG AAC TCC AAA TTT
Ile Val Leu Glu Pro Ile Tyr Trp Asn Ser Ser Asn Ser Lys Phe>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

     140     150     160     170     180
      *      *      *      *      *
CTA CCC GGA CAA GGC CTG GTA CTA TAC CCA CAG ATA GGA GAC AAA
Leu Pro Gly Gln Gly Leu Val Leu Tyr Pro Gln Ile Gly Asp Lys>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

     190     200     210     220
      *      *      *      *      *
TTG GAT ATT ATT TGC CCC AAA GTG GAC TCT AAA ACT GTT GGC CAG
Leu Asp Ile Ile Cys Pro Lys Val Asp Ser Lys Thr Val Gly Gln>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

     230     240     250     260     270
      *      *      *      *      *
TAT GAA TAT TAT AAA GTT TAT ATG GTT GAT AAA GAC CAA GCA GAC
Tyr Glu Tyr Tyr Lys Val Tyr Met Val Asp Lys Asp Gln Ala Asp>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

     280     290     300     310
      *      *      *      *      *
AGA TGC ACA ATT AAG AAG GAG AAT ACC CCG CTG CTC AAC TGT GCC
Arg Cys Thr Ile Lys Lys Glu Asn Thr Pro Leu Leu Asn Cys Ala>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

     320     330     340     350     360
      *      *      *      *      *
AGA CCA GAC CAA GAT GTG AAA TTC ACC ATC AAG TTT CAA GAA TTC
Arg Pro Asp Gln Asp Val Lys Phe Thr Ile Lys Phe Gln Glu Phe>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

     370     380     390     400
      *      *      *      *      *
AGC CCT AAC CTC TGG GGT CTA GAA TTT CAG AAG AAC AAA GAT TAC
Ser Pro Asn Leu Trp Gly Leu Glu Phe Gln Lys Asn Lys Asp Tyr>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE) __a__>

```

Fig.15B.

```

      410      420      430      440      450
      *      *      *      *      *
TAC ATT ATA TCT ACA TCA AAT GGG TCT TTG GAG GGC CTG GAT AAC
Tyr Ile Ile Ser Thr Ser Asn Gly Ser Leu Glu Gly Leu Asp Asn>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

      460      470      480      490
      *      *      *      *      *
CAG GAG GGA GGG GTG TGC CAG ACA AGA GCC ATG AAG ATC CTC ATG
Gln Glu Gly Gly Val Cys Gln Thr Arg Ala Met Lys Ile Leu Met>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

      500      510      520      530      540
      *      *      *      *      *
AAA GTT GGA CAA GAT GCA AGT TCT GCT GGA TCA GCC AGG AAT CAC
Lys Val Gly Gln Asp Ala Ser Ser Ala Gly Ser Ala Arg Asn His>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

      550      560      570      580
      *      *      *      *      *
GGT CCA ACA AGA CGT CCA GAG CTA GAA GCT GGT ACA AAT GGG AGA
Gly Pro Thr Arg Arg Pro Glu Leu Glu Ala Gly Thr Asn Gly Arg>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

      590      600      610      620      630
      *      *      *      *      *
AGT TCA ACA ACA AGT CCC TTT GTG AAG CCA AAT CCA GGT TCT AGC
Ser Ser Thr Thr Ser Pro Phe Val Lys Pro Asn Pro Gly Ser Ser>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

      640      650      660      670
      *      *      *      *      *
ACC GAT GGC AAC AGC GCG GGG CAT TCC GGG AAC AAT CTC CTG GGG
Thr Asp Gly Asn Ser Ala Gly His Ser Gly Asn Asn Leu Leu Gly>
__a__EPHRIN-B2  ECTO DOMAIN 1 (WITH SIGNAL PEPTIDE)__a__>

      680      690      700      710      720
      *      *      *      *      *
GGC CCG GGA ATA GTT TTA GAG CCT ATC TAC TGG AAT TCC TCG AAC
Gly Pro Gly>
__b__b__>
      Ile Val Leu Glu Pro Ile Tyr Trp Asn Ser Ser Asn>
      __EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNA__>

      730      740      750      760
      *      *      *      *      *
TCC AAA TTT CTA CCC GGA CAA GGC CTG GTA CTA TAC CCA CAG ATA
Ser Lys Phe Leu Pro Gly Gln Gly Leu Val Leu Tyr Pro Gln Ile>
__EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e__>

      770      780      790      800      810
      *      *      *      *      *
GGA GAC AAA TTG GAT ATT ATT TGC CCC AAA GTG GAC TCT AAA ACT
Gly Asp Lys Leu Asp Ile Ile Cys Pro Lys Val Asp Ser Lys Thr>
__EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e__>

```

Fig.15C.

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      820      830      840      850
      *      *      *      *
GTT GGC CAG TAT GAA TAT TAT AAA GTT TAT ATG GTT GAT AAA GAC
Val Gly Gln Tyr Glu Tyr Tyr Lys Val Tyr Met Val Asp Lys Asp>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      860      870      880      890      900
      *      *      *      *      *
CAA GCA GAC AGA TGC ACA ATT AAG AAG GAG AAT ACC CCG CTG CTC
Gln Ala Asp Arg Cys Thr Ile Lys Lys Glu Asn Thr Pro Leu Leu>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      910      920      930      940
      *      *      *      *      *
AAC TGT GCC AGA CCA GAC CAA GAT GTG AAA TTC ACC ATC AAG TTT
Asn Cys Ala Arg Pro Asp Gln Asp Val Lys Phe Thr Ile Lys Phe>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      950      960      970      980      990
      *      *      *      *      *
CAA GAA TTC AGC CCT AAC CTC TGG GGT CTA GAA TTT CAG AAG AAC
Gln Glu Phe Ser Pro Asn Leu Trp Gly Leu Glu Phe Gln Lys Asn>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      1000     1010     1020     1030
      *      *      *      *      *
AAA GAT TAC TAC ATT ATA TCT ACA TCA AAT GGG TCT TTG GAG GGC
Lys Asp Tyr Tyr Ile Ile Ser Thr Ser Asn Gly Ser Leu Glu Gly>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      1040     1050     1060     1070     1080
      *      *      *      *      *
CTG GAT AAC CAG GAG GGA GGG GTG TGC CAG ACA AGA GCC ATG AAG
Leu Asp Asn Gln Glu Gly Gly Val Cys Gln Thr Arg Ala Met Lys>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      1090     1100     1110     1120
      *      *      *      *      *
ATC CTC ATG AAA GTT GGA CAA GAT GCA AGT TCT GCT GGA TCA GCC
Ile Leu Met Lys Val Gly Gln Asp Ala Ser Ser Ala Gly Ser Ala>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      1130     1140     1150     1160     1170
      *      *      *      *      *
AGG AAT CAC GGT CCA ACA AGA CGC CCA GAG CTA GAA GCT GGT ACA
Arg Asn His Gly Pro Thr Arg Arg Pro Glu Leu Glu Ala Gly Thr>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      1180     1190     1200     1210
      *      *      *      *      *
AAT GGG AGA AGT TCA ACA ACA AGT CCC TTT GTG AAG CCA AAT CCA
Asn Gly Arg Ser Ser Thr Thr Ser Pro Phe Val Lys Pro Asn Pro>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

      1220     1230     1240     1250     1260
      *      *      *      *      *
GGT TCT AGC ACC GAT GGC AAC AGC GCG GGG CAT TCC GGG AAC AAT
Gly Ser Ser Thr Asp Gly Asn Ser Ala Gly His Ser Gly Asn Asn>
____EPHRIN-B2  ECTO DOMAIN 2 ( WITHOUT SIGNAL PEPTIDE)_e____>

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Fig.15D.

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      1270      1280      1290      1300
      *        *        *        *        *        *        *        *
CTC CTG GGG G GC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC
      Glu Pro Lys Ser Cys Asp Lys Thr His>
      ____c____HUMAN IGG1 FC TAG__c__c__>

      Gly Pro Gly>
      _d_d_d__>
Leu Leu Gly Xxx>
__e__e__e__>

      1310      1320      1330      1340      1350
      *        *        *        *        *        *        *        *
ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser>
__c__c__c__c__c____HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1360      1370      1380      1390
      *        *        *        *        *        *        *        *
GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser>
__c__c__c__c__c____HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1400      1410      1420      1430      1440
      *        *        *        *        *        *        *        *
CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu>
__c__c__c__c__c____HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1450      1460      1470      1480
      *        *        *        *        *        *        *        *
GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val>
__c__c__c__c__c____HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1490      1500      1510      1520      1530
      *        *        *        *        *        *        *        *
CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr>
__c__c__c__c__c____HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1540      1550      1560      1570
      *        *        *        *        *        *        *        *
TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu>
__c__c__c__c__c____HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1580      1590      1600      1610      1620
      *        *        *        *        *        *        *        *
AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro>
__c__c__c__c__c____HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1630      1640      1650      1660
      *        *        *        *        *        *        *        *
CCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg>
__c__c__c__c__c____HUMAN IGG1 FC TAG__c__c__c__c__c__>

```

Fig.15E.

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1670      1680      1690      1700      1710
  *      *      *      *      *
GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr>
__c__c__c__c__c__HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1720      1730      1740      1750
  *      *      *      *      *
AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro>
__c__c__c__c__c__HUMAN IGG1 FC TAG__c__c__c__c__c__>

1760      1770      1780      1790      1800
  *      *      *      *      *
AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn>
__c__c__c__c__c__HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1810      1820      1830      1840
  *      *      *      *      *
AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe>
__c__c__c__c__c__HUMAN IGG1 FC TAG__c__c__c__c__c__>

1850      1860      1870      1880      1890
  *      *      *      *      *
TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln>
__c__c__c__c__c__HUMAN IGG1 FC TAG__c__c__c__c__c__>

      1900      1910      1920      1930
  *      *      *      *      *
GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn>
__c__c__c__c__c__HUMAN IGG1 FC TAG__c__c__c__c__c__>

1940      1950      1960      1970
  *      *      *      *      *
CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>
__c__c__c__c__c__HUMAN IGG1 FC TAG__c__c__c__c__c__>

```

Fig.16.

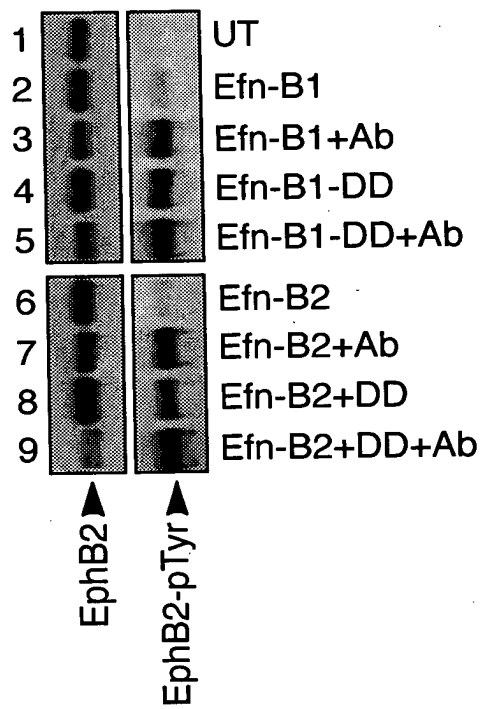


Fig.17.

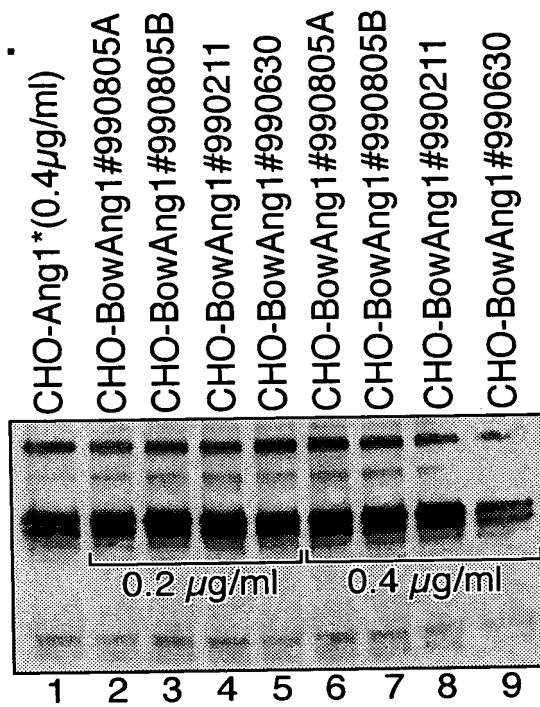


Fig.18.

